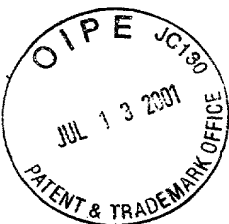


#1



T001740"2221260

	1		50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVATAVLA TLLFATVQAS.
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA SATV-TAVLA TLL-ATVQA-</u>

C1

	51		100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRIVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG NGENE.STGN IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSAL	VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	-----	-L--V-R---	V-----EG --E-E-----

V1

	101		150
EG327	GVLTAGTITL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSS ....FTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSTYSLK KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSTYSLK KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN... ....FTYSLK KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN... ....FTYSLK KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNNTNENT NDSSTYSLK KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD..... ....FTYSLK KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTGILNVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTGILNVE
Consensus	-----TL	<u>KAGDNLKIKQ</u>	-----FTYSLK K-L--L--V-

V1

C2

V2

C3

FIG. 1

	151		200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE TNGDPTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNI-SDTK</u>	<u>GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L</u>

C3

	201		250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDKKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVP GTTAS..DNV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVP GTTAS..DNV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
Consensus	<u>----A-----</u>	<u>----T-----</u>	<u>RAAS-KDVLN AGWNIKGVP G-T-----NV</u>

V3

C4

V4

	251		300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGKL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGKL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGKL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGKL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGKL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGKL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGKL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGKL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGKL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGKL
Consensus	<u>DFV-TYDTVE</u>	<u>FLSADTKTTT</u>	<u>VNVESKDNGK -TEVKIGAKT SVIKEKDGKL</u>

C5

**FIG. 1**

	301		350
EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ198	VTGKGKDENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ10	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H15	VTGKGKDENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
EG329	VTGKDKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
PMC21	VTGKDKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H38	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
P20	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Z2491	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H41	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN KAGWRMKTTT ANGQTGQADK</u>

C5

	351		400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Consensus	<u>FETVTSGT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGNI TV-YDVNVGD ALNVNQLQNS</u>

C5

	401		450
EG327	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ10	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H15	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H38	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
P20	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EISRNGKNID
H41	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus	<u>GWNLDKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>

C5

**FIG. 1**

451 500

EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

501 550

EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

551 600

EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

**FIG. 1**

	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

**FIG. 1**

	1						70
H15	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ10	ATGAACAAAA	TATCCCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ198	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
P20	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	AGTCGTATCC	GAGCTCACAC
H38	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Z2491	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
H41	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
EG329	ATGAACGAAA	TATTGCGCAT	CATTGGAAT	AGCGCCCTCA	ATGCCTGGGT	CGTTGTATCC	GAGCTCACAC
PMC21	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC
EG327	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Consensus	<u>ATGAAC-AAA</u>	<u>TAT--CGCAT</u>	<u>CATTGGAAT</u>	<u>AG-GCCCTCA</u>	<u>ATGC-TGGGT</u>	<u>-G--GTATCC</u>	<u>GAGCTCACAC</u>

C1

	71						140
H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ10	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGCTGT	CCGCAACGGT
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACGCTGTTGT	TTGCAACGGT
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
Consensus	<u>GCAACCACAC</u>	<u>CAAACGCGCC</u>	<u>TCCGCAACCG</u>	<u>TG--GACCGC</u>	<u>CGTATTGGCG</u>	<u>AC-CTG-TGT</u>	<u>--GCAACGGT</u>

C1

	141						210
H15	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ10	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ198	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
P20	TCAGGCGAAT	GCTACCGATA	CCGAT.....	.GAAGATGAA	GAGTTAGAA	CCGTAGCACG	CTCTGCTCTG
H38	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAAC	CCGTAGTACG	CTCTGCTCTG
Z2491	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGCTGTA
H41	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTG...TC
EG329	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTGCTACG	CACTGTTGCC
PMC21	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CACTGTTGCC
EG327	TCAGGCGAGT	ACTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
Consensus	<u>TCAGGC-A-T</u>	<u>-CTA-C-AT-</u>	<u>--GA-----</u>	<u>----GA---A</u>	<u>-A-TTAGA--</u>	<u>CCGT---ACG</u>	<u>C-CTG----</u>

C1

V1

FIG. 2

211 280

H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ10	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA
Z2491	GGG..AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGC GAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCGAAT	TGGAAACGAT	A.....	TCATTATCAA
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----	-----

V1

281 350

H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA... .	.GTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
EG327	GAGTATATTT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
Consensus	-----A---	-----	-----	-----	--T-ACCCTC	AAAGCCGGCG	ACAACCTGAA

V1

C2

351 420

H15	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ10	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ198	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
P20	AATCAAACAA	AGCGGCAAG	A.....	.....	.....	.CTTCACCTA	CTCGCTGAAA
H38	AATCAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA
Z2491	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
H41	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
EG329	AATCAAACAA	AAC.....	.....G..	.....	....GCACAA	ACTTCACCTA	CTCGCTGAAA
PMC21	AATCAAACAA	AAC.....	.....G..	.....	....GCACAA	ACTTCACCTA	CTCGCTGAAA
EG327	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
Consensus	AATCAAACAA	A-C-----	-----	-----	-----	-CTTCACCTA	CTC-CTGAAA

C2

V2

C3

FIG. 2

421 490

H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
P20	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
Z2491	AAAGACCTCA	CAGGCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
H41	AAAGACCTCA	CAGGCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
Consensus	<u>AAAGA-CT-A</u>	<u>-AG--CTGA-</u>	<u>CA-TGTTG-A</u>	<u>ACTGAAAAAT</u>	<u>TATCGTTT-G</u>	<u>CGCAAAC-G-</u>	<u>AA-AAAGTCA</u>

C3

491 560

H15	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ10	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ198	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
P20	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
H38	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
Z2491	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
H41	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
EG329	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
PMC21	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
EG327	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
Consensus	<u>ACATCA-AAG</u>	<u>CGACACCAAA</u>	<u>GGCTTGAATT</u>	<u>T-GCGAAA-A</u>	<u>AACGGCTG-G</u>	<u>AC-AACGGCG</u>	<u>AC-CCACGGT</u>

C3

561 630

H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
H38	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG329	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
PMC21	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Consensus	<u>TCATCTGAAC</u>	<u>GGTAT-GGTT</u>	<u>CGACTTTGAC</u>	<u>CGATA-GCT-</u>	<u>--G--T-C--</u>	<u>--GC--C---</u>	<u>----G---C-</u>

C3

V3

FIG.2



	631						700
H15	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAGGA	TGTGTTGAAT	GCGGGTTGGA
H38	AACGACAACG	TTACCGATGA	CAAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAGGA	TGTGTTGAAT	GCGGGTTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	---AC-A--	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA
		V3			C4		
	701						770
H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTC	GATTTCGTCC	GCACCTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
P20	ATATTAAGGG	TGTTAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACCTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
Z2491	ATATTAAGGG	TGTTAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACCTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACCTACGA
Consensus	A-ATTAA-GG	-GTTAAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCGTCC	-CACTTACGA
	C4		V4			C5	
	771						840
H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
				C5			
	841						910
H15	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AGAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AGAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AGAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AGAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AGAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATCA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTAT-A	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
				C5			

FIG. 2

911 980

H15	AAGGCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ10	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ198	AAGGCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
P20	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H38	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Z2491	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H41	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG329	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
PMC21	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG327	AAGACAAAGG	CGAGAATGAT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Consensus	<u>AAG-CAAAG-</u>	<u>CGAGAATG-T</u>	<u>TCTTCTACAG</u>	<u>AC-AAGGCCA</u>	<u>AGGCTTAGTG</u>	<u>ACTGCAAAAG</u>	<u>AAGTGATTGA</u>

C5

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ10	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	<u>TGCAGTAAAC</u>	<u>AAGGCTGGTT</u>	<u>GGAGAATGAA</u>	<u>AACAACAACC</u>	<u>GCTAATGGTC</u>	<u>AAACAGGTCA</u>	<u>AGCTGACAAG</u>

C5

1051 1120

H15	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
BZ10	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
BZ198	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
P20	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
H38	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
Z2491	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
H41	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
EG329	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
PMC21	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
EG327	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAAC TGCG	ACTGTAAGTA
Consensus	<u>TTTGAAACCG</u>	<u>TTACATCAGG</u>	<u>CACAAA-GTA</u>	<u>ACCTTTGCTA</u>	<u>GTGGTAA-GG</u>	<u>TACAAC TGCG</u>	<u>ACTGTAAGTA</u>

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ10	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	<u>AAGATGATCA</u>	<u>AGGCAACATC</u>	<u>ACTGTTA-GT</u>	<u>ATGATGTAAA</u>	<u>TGTCGGCGAT</u>	<u>GCCCTAAACG</u>	<u>TCAATCAGCT</u>

C5

FIG. 2

1191 1260

H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ10	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	<u>GCAAAACAGC</u>	<u>GGTTGGAATT</u>	<u>TGGATTCCAA</u>	<u>AGCGGTTGCA</u>	<u>GGTCTTCGG</u>	<u>GCAAAGTCAT</u>	<u>CAGCGGCAAT</u>

C5

1261 1330

H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ10	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	<u>GTTTCGCCGA</u>	<u>GCAAGGGAAA</u>	<u>GATGGATGAA</u>	<u>ACCGTCAACA</u>	<u>TTAATGCCGG</u>	<u>CAACAACATC</u>	<u>GAGATTACCC</u>

C5

1331 1400

H15	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
BZ10	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
BZ198	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
P20	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
H38	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
Z2491	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
H41	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
EG329	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
PMC21	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
EG327	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
Consensus	<u>GCAACGG-AA</u>	<u>AAATATCGAC</u>	<u>ATCGCCACTT</u>	<u>CGATG-C-CC</u>	<u>GCA-TTTTCC</u>	<u>AGCGTTTCGC</u>	<u>TCGG-CGCGG</u>

C5

1401 1470

H15	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ10	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ198	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
P20	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H38	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Z2491	GGCAGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H41	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
EG329	GGCGGATGCG	CCCACTTTGA	GCGTGGAT..	GGGGACGCA	TTGAATGTCG	GCAGCAAGAA	GGACAACAAA
PMC21	GGCGGATGCG	CCCACTTTGA	GCGTGGAT..	GGGGACGCA	TTGAATGTCG	GCAGCAAGAA	GGACAACAAA
EG327	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Consensus	<u>GGC-GATGCG</u>	<u>CCCACTTT-A</u>	<u>GCGTGGAT--</u>	<u>---GG-CGC-</u>	<u>TTGAATGTCG</u>	<u>GCAGCAAG-A</u>	<u>---CAACAAA</u>

C5

FIG. 2

12/31

	1471							1540
H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
BZ10	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
BZ198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCG	CAACTTAAAG	
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTTAAAGAGG</u>	<u>GGGATGTTAC</u>	<u>AAACGTCGC-</u>	<u>CAACTTAAAG</u>	

C5

	1541							1610
H15	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
BZ10	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
BZ198	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
P20	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
H38	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
Z2491	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
H41	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
EG329	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
PMC21	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
EG327	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
Consensus	<u>G-GTGGCGCA</u>	<u>AAACTTGAAC</u>	<u>AACC-CATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGCG</u>	<u>CG-GCGGG-A</u>	<u>TCGCCCAAGC</u>	

C5

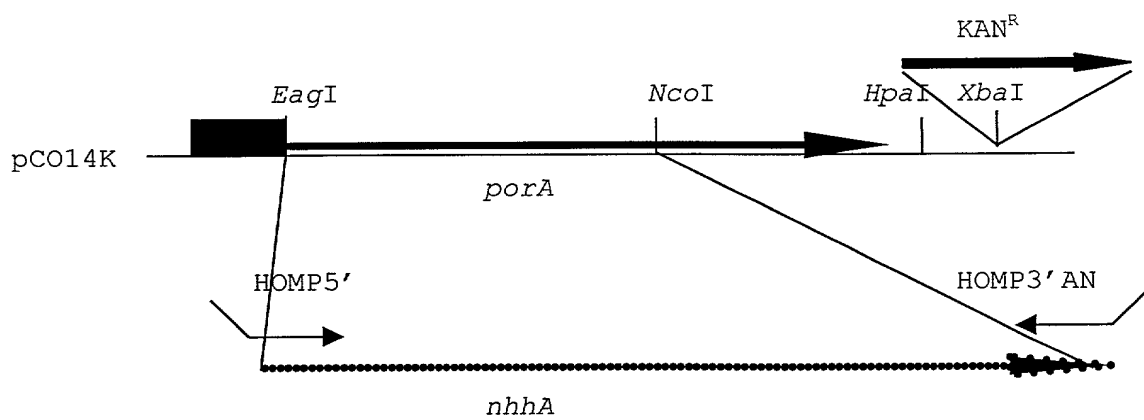
	1611							1680
H15	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
BZ10	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
BZ198	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACACT	
P20	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
H38	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
Z2491	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
H41	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
EG329	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
PMC21	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
EG327	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT	
Consensus	<u>GATTGCAACC</u>	<u>GCAGGT-T-G</u>	<u>-TCAGGC-TA</u>	<u>T-TGCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGGCG--ACT</u>	

C5

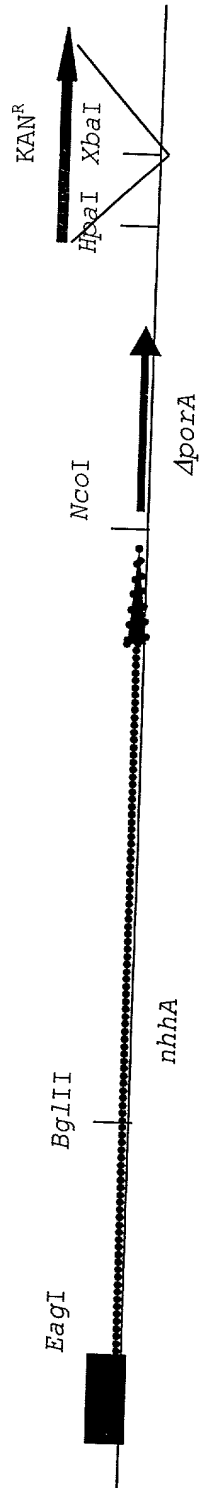
**FIG. 2**

**FIG. 2**

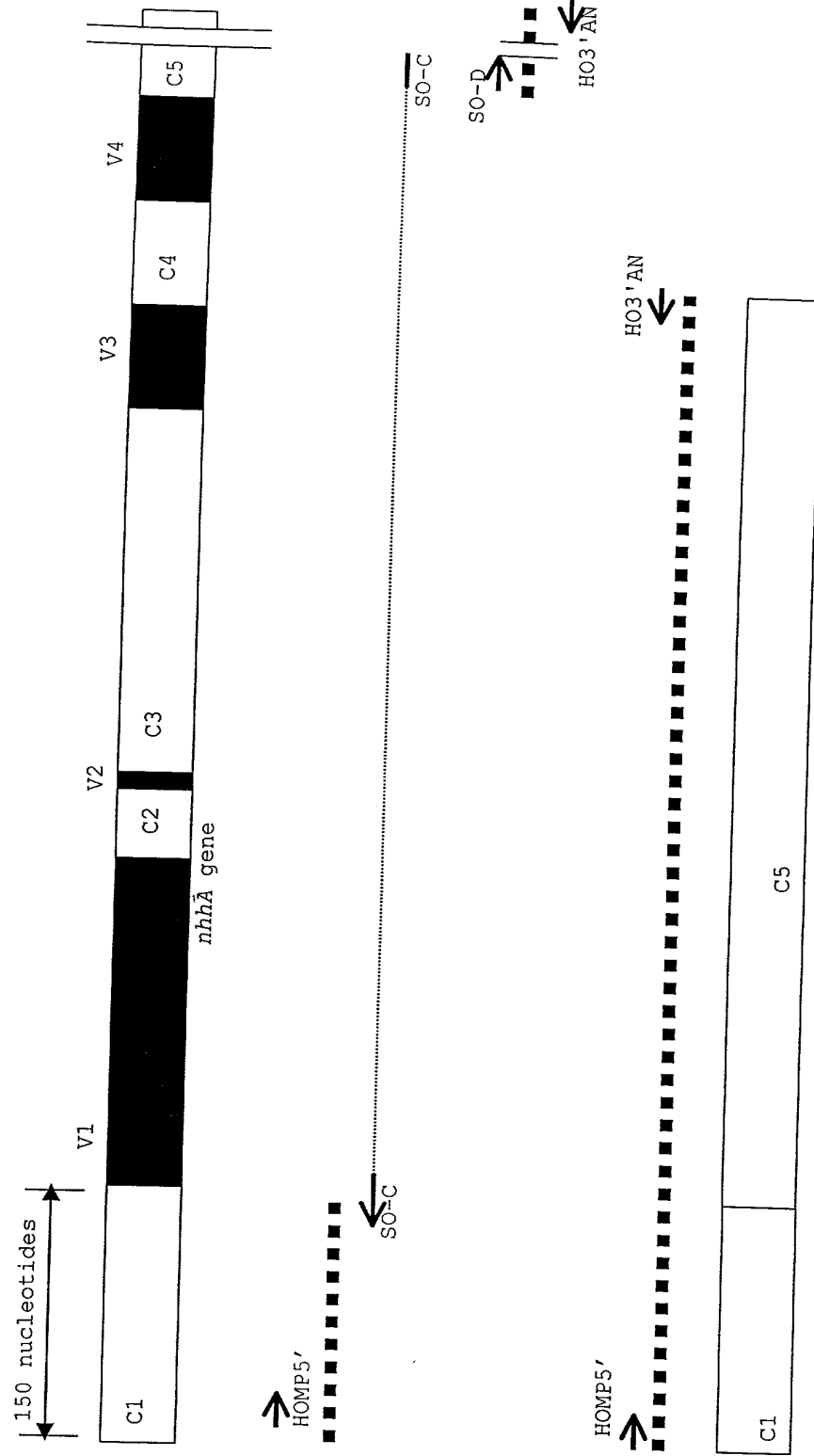
	1751	1815
H15	GCAcGGCTTC	CGGCAATTcG
BZ10	GCACGGCTTC	CGGCAATTcG
BZ198	GCACGGCTTC	CGGCAATTcG
P20	GCACGGCTTC	CGGCAATTcG
H38	GCACGGCTTC	CGGCAATTcG
Z2491	GCACGGCTTC	CGGCAATTcG
H41	GCACGGCTTC	CGGCAATTcG
EG329	GCACGGCTTC	CGGCAATTcG
PMC21	GCACGGCTTC	CGGCAATTcG
EG327	GCACGGCTTC	CGGCAATTcG
Consensus	GCACGGCTTC	CGGCAATTcG

**FIG. 3A**

PIP52 (PMC21)



**FIG. 3B**



**FIG. 4A**





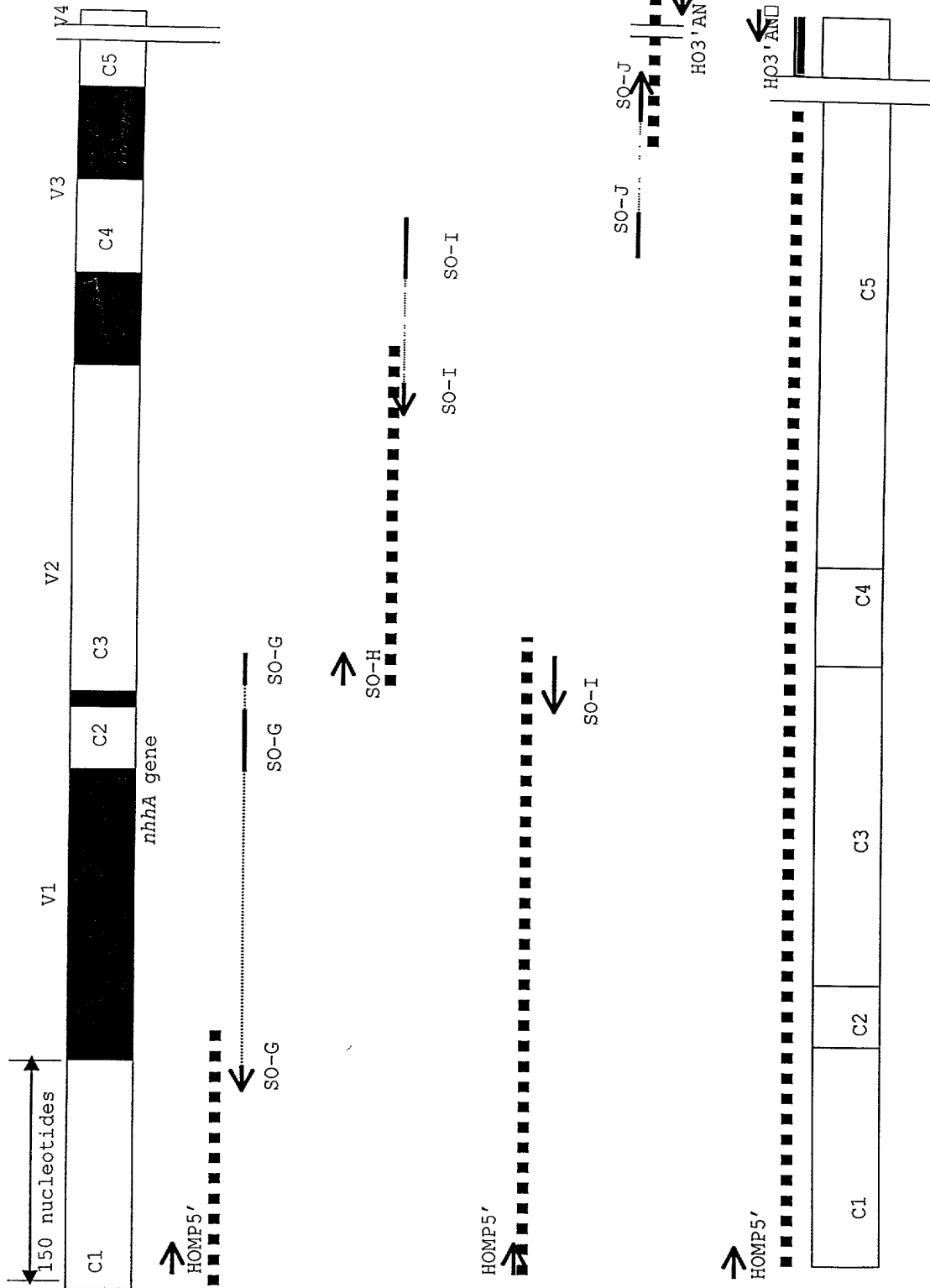


FIG. 4C

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TT VHL  
 101 NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK  
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT TTA  
 251 NGQTGQADKF ETVTSGTNTV FASGKGTTAT VSKDDQGNIT VMYDVNVGDA  
 301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE  
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV  
 401 RITNVAPGVK EGDVTNVAQL KGVAQN LNNR IDNVDGNARA GIAQAIATAG  
 451 LVQAYLP GKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KG TASGNSRG  
 501 HFGASASVG Y QW\*

## FIG. 5A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACAAATG AAACAGATCT GACCAAGTGT GGAAC TGAA AATTATCGTT  
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA  
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG  
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC  
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG  
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA  
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC  
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGA  
 551 GCAAAGACAA CCGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT  
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAAGGCGA  
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAGAAG  
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACACCGCT  
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC  
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG  
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC  
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTTGG ATTCCAAGC  
 951 GGTTCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA  
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG  
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA  
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG  
 1151 TGGATGGGGA CGCATTTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC  
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT  
 1251 CGCACAACTT AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG  
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACCGCAGGT  
 1351 CTGGTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG  
 1401 CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG  
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGG  
 1501 CATTTCCGGTG CTTCCGCATC TGTCGGTTAT CAGTGGTAA

## FIG. 5B

```

1  MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
51  ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTDM LLNTGATTNV TNDNVTDDDEK KRAASVKDVL NAGWNIKGVK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKKDGKLV TGKKGGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDDET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501 GHFGASASVG YQW*

```

**FIG. 6A**

```

1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT
51  CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACGTGTGTGT TTGCAACGGT TCAGGCGAAT
151 GCTACCGATG AAACAGGCCCT GATCAATGTT GAAACTGAAA AATTATCGTT
201 TGGCGCAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
251 ATTTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAGAAG
701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAACCGCT
751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
1201 GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA
1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
1351 GGTCTGGTTC AGGCGTATCT GCCC GGCAAG AGTATGATGG CGATCGGCGG
1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTCGCGC
1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

```

**FIG. 6B**

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAFLA TLLFATVQAS  
 51 ANNVDVFRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK  
 101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG  
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ  
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDET VNINA GNNIEITRNG  
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRIITNV  
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY  
 351 LPGKSMAAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS  
 401 ASVGyQW\*

## FIG. 7A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACAAAC TTGATTTTCT CCGCACTTAC GACACAGTCG AGTTCCTTGAG  
 201 CGCAGATACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA  
 251 AGAAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAA  
 301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC  
 351 AGACGAAGGC GAAGGCTTAG TGAAGTGAAG AGAAGTGATT GATGCAGTAA  
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAAACAGGT  
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC  
 501 TAGTGGTAAA GGTACAACCTG CGACTGTAAG TAAAGATGAT CAAGGCAACA  
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG  
 601 CTGCAAAACA GCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC  
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG  
 701 AAACCGTCAA CATTAAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT  
 751 AAAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC  
 801 GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT  
 851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC  
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG  
 951 CGTGCGCGAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC  
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT  
 1051 TTGCCCCGGA AGAGTATGAT GCGGATCGGC GCGGCGACTT ATCGCGGCGA  
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA  
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CGGTGCTTCC  
 1201 GCATCTGTCG GTTATCAGTG GTAA

## FIG. 7B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT  
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV  
 151 TAKEVIDAVN KAGWRMKTTT ANGQTQADK FETVTSGTNV TFASGKGTTA  
 201 TVSKDDQGNi TVMYDVNVGD ALNVNQLQNS GWNLD SKAVA GSSGKVISGN  
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA  
 301 PTLSDVDG DAL NVGSKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN  
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLP GK SMMAIGGGTY RGEAGYAIGY  
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW\*

## FIG. 8A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT  
 201 TAAAGGCGTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTTCGTCC  
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT  
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAATCGG  
 351 TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG  
 451 ACTGCAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA  
 501 AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG  
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG  
 601 ACTGTAAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA  
 651 TGTCGGCGAT GCCCTAAACG TCAATCAGCT GCAAAAACAGC GGTTGGAATT  
 701 TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT  
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCCG  
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT  
 851 CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG GGCGGATGCG  
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA  
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG  
 1001 ATGTTACAAA CGTCGCACAA CTTAAAGGCG TGGCGCAAAA CTTGAACAAC  
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT  
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCCCGCAAG AGTATGATGG  
 1151 CGATCGGCGG CGGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC  
 1201 TCCAGTATTT CCGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG  
 1251 CAATTCGCGC GGCCATTTCC GTGCTTCCGC ATCTGTGGT TATCAGTGGT  
 1301 AA

## FIG. 8B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK  
 101 GLNEAKETAG TNGDTTVHLN GIGSTLTDRASVVKDVLNAG WNIKGVKNVD  
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEDGKLV  
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT'TTA NGQTGQADKF  
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG  
 301 WNLDISKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI  
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK  
 401 EGDVTNVAQL KGVAQNLLNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS  
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY  
 501 QW\*

## FIG. 9A

1 ATGAACAAAA TATACCGCAT CATT'TGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTACCTA  
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGT'TGGA ACTGAAAAAT  
 251 TATCGTTTAG CGCAAACGGC AATAAAGTCA ACATCACAAG CGACACCAAA  
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT  
 351 TCATCTGAAC GGTATTGGTT CGACTT'TGAC CGATCGTGCG GCAAGCGTTA  
 401 AAGACGTATT AAACGCTGGC TGGAACATTA AAGGCGTTAA AAACGTTGAT  
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC  
 501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA  
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT  
 601 ACTGGTAAAG ACAAAGGCGA GAATGGTTCT TCTACAGACG AAGGCGAAGG  
 651 CTTAGTGACT GCAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA  
 701 GAATGAAAAC AACAACCGCT AATGGTCAA CAGGTCAAGC TGACAAGTTT  
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC  
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG  
 851 ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT  
 901 TGGAATTTGG ATTCCAAAGC GGTTGCAGGT TCTTCGGGCA AAGTCATCAG  
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA  
 1001 ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC  
 1051 GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC  
 1101 GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA  
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA  
 1201 GAGGGGGATG TTACAAACGT CGCACAACCT AAAGGCGTGG CGCAAACTT  
 1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC  
 1301 AAGCGATTGC AACCGCAGGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT  
 1351 ATGATGGCGA TCGGCGGCGG CACTTATCGC GGCGAAGCCG GTTACGCCAT  
 1401 CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG  
 1451 CTTCCGGCAA TTCGCGCGGC CATTTCCGGT CTTCCGCATC TGTCGGTTAT  
 1501 CAGTGGTAA

## FIG. 9B

	1				50
H41	<u>MNKIYRIWN</u>	<u>SALNAWVAVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAN</u>
PMC21	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>DLTRNHTKRA</u>	<u>SATVNTAVLA</u>	<u>TLLFATVOAS</u>
H41Studel	<u>MNKIYRIWN</u>	<u>SALNAWVAVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAN</u>
PMC21Bgldel	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAS</u>
PMC21C1C5	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAS</u>
	C1				
	51				100
H41	<u>ATDED...EEE</u>	<u>ELESVQRS.V</u>	<u>VGSIQASMEG</u>	<u>SVELET...I</u>	<u>SLSMTNDSKE</u>
PMC21	<u>ANNEEQEYI</u>	<u>YLHPVORTVA</u>	<u>VLIVNSDKEG</u>	<u>AGEKEKVEEN</u>	<u>SDWAVYFNEK</u>
H41Studel	<u>ATDE.....</u>				
PMC21Bgldel	<u>ANNE.....</u>				
PMC21C1C5	<u>AN.....</u>				
	V1				
	101				150
H41	<u>FVDPYIVVTL</u>	<u>KAGDNLKIKO</u>	<u>N.TNENTNAS</u>	<u>SFTYSLKKDL</u>	<u>TGLINVETEK</u>
PMC21	<u>GVLTAIREITL</u>	<u>KAGDNLKIKO</u>	<u>NGTN.....</u>	<u>.FTYSLKKDL</u>	<u>TDLTSVGTEK</u>
H41Studel					<u>TGLINVETEK</u>
PMC21Bgldel					<u>TDLTSVGTEK</u>
PMC21C1C5					
	V1	C2	V2	C3	
	151				200
H41	<u>LSFGANGKKV</u>	<u>NIISDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDMLLNT</u>
PMC21	<u>LSFSAHGNKV</u>	<u>NITSDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDLLNT</u>
H41Studel	<u>LSFGANGKKV</u>	<u>NIISDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDMLLNT</u>
PMC21Bgldel	<u>LSFSAHGNKV</u>	<u>NITSDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDLLNT</u>
PMC21C1C5					
		C3		V3	
	201				250
H41	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
H41Studel	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21Bgldel	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21C1C5					<u>...NVDFVRT</u>
	V3	C4	V4	C5	
	251				300
H41	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGK</u>
PMC21	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
H41Studel	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGK</u>
PMC21Bgldel	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
PMC21C1C5	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
	C5				
	301				350
H41	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
H41Studel	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21Bgldel	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21C1C5	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
	C5				
	351				400
H41	<u>SGTKVTFASG</u>	<u>NGTTATVSKD</u>	<u>DOGNITVKYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
H41Studel	<u>SGTKVTFASG</u>	<u>NGTTATVSKD</u>	<u>DOGNITVKYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21Bgldel	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21C1C5	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
	C5				

FIG. 10



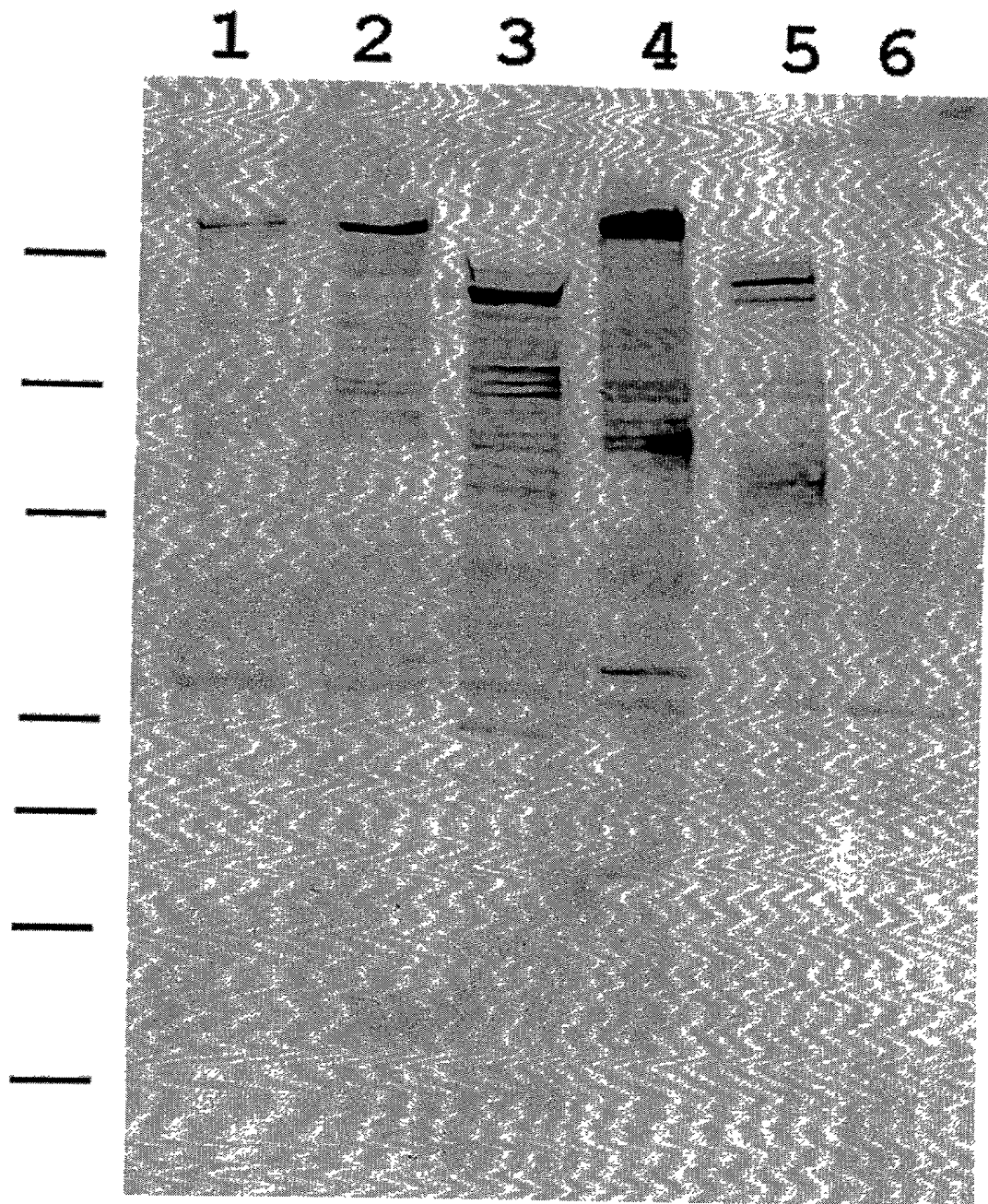
401 450  
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
C5

451 500  
H41 TPOFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD  
PMC21 TPOFSSVSLG AGADAPTLVS DG.DALNVGS KKDNPVRLT NVAPGVKEGD  
H41Studel TPOFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD  
PMC21Bgldel TPOFSSVSLG AGADAPTLVS DG.DALNVGS KKDNPVRLT NVAPGVKEGD  
PMC21C1C5 TPOFSSVSLG AGADAPTLVS DG.DALNVGS KKDNPVRLT NVAPGVKEGD  
C5

501 550  
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA  
PMC21 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA  
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA  
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA  
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA  
C5

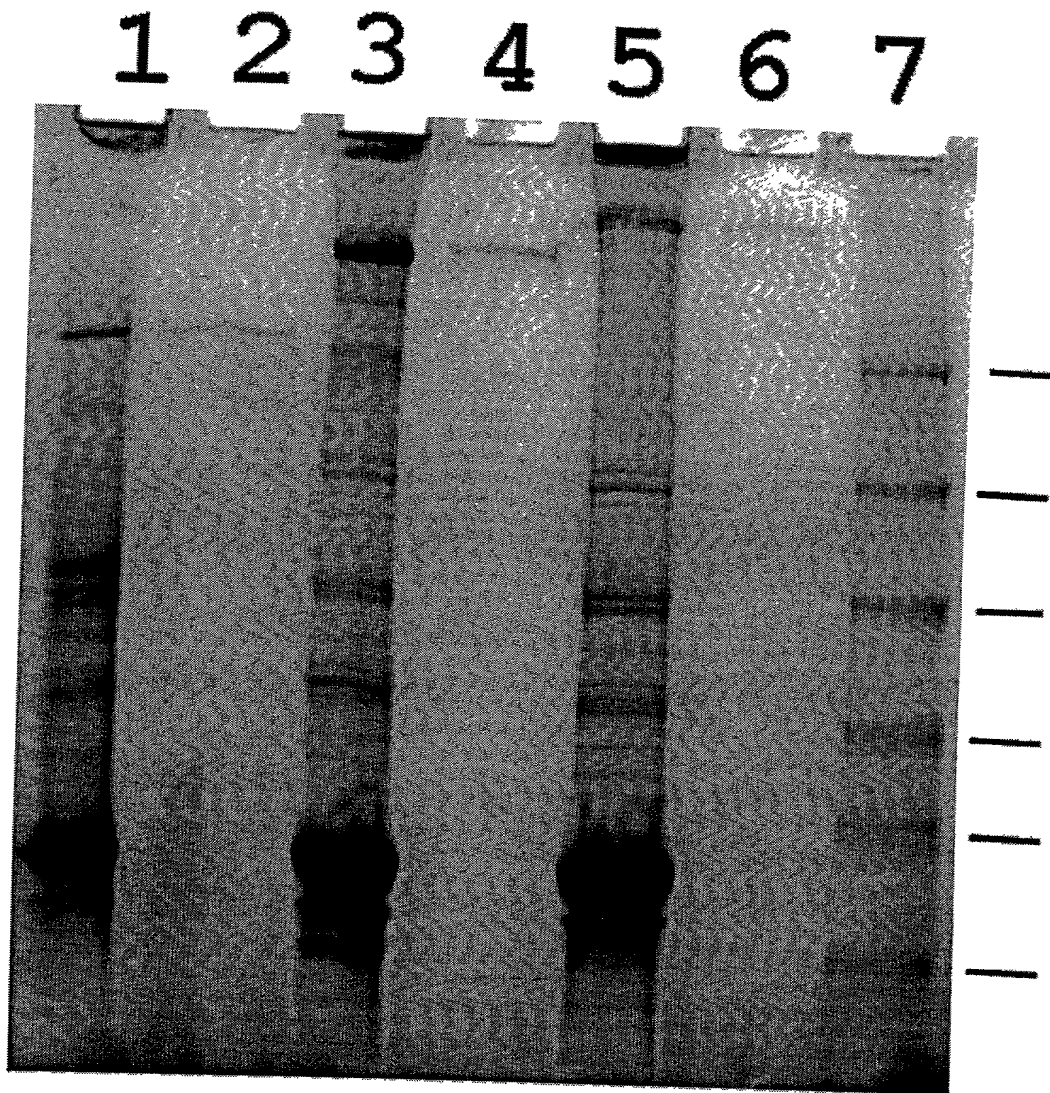
551 600  
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.  
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYQW.  
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.  
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYQW.  
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYQW.  
C5

**FIG. 10**



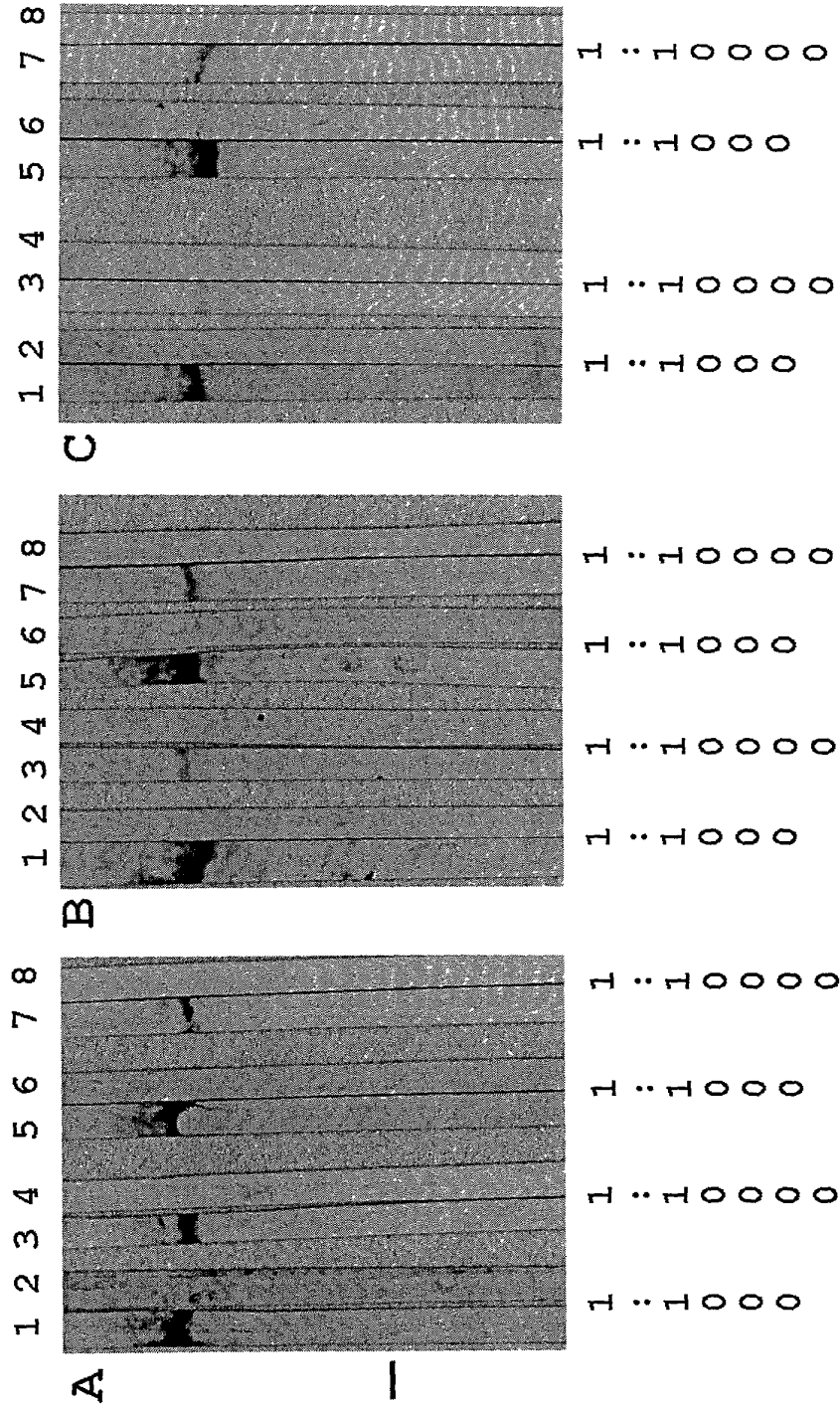
**FIG. 11**

097488 0930  
T0E T40" 288T/260



**FIG. 12**

TOCT-0288T/60



173—  
**FIG. 13**

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK  
 101 GVLTAAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG  
 151 NKVNITS DTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT  
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL  
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS  
 301 TDEGEGLVTA KEVIDAVNKA GWRMKT TAN GTTGQADKFE TVTSGTNVTF  
 351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS  
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV  
 451 SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK  
 501 GVAQNLNNRI DNV DGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG  
 551 EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVG YQ W\*

## FIG. 14A

52 TDEDEEEEL ESVQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI  
 101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG  
 151 KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT  
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL  
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS  
 301 TDEGEGLVTA KEVIDAVNKA GWRMKT TAN GTTGQADKFE TVTSGTKVTF  
 351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS  
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV  
 451 SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL  
 501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL  
 551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVG Y QW\*

## FIG. 14B

52 NNETDLTSV GTEKLSFSAN GNKVNITSdT KGLNFAKETA GTNGDttVHL  
 101 NGIGSTLTDT LLNTGATTNV TNDNVTdDEK KRAASVKDVL NAGWNIKGVK  
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA  
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA  
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMDet VNINAGNNIE  
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV  
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVdGNARA GIAQAIATAG  
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGtASGNSRG  
 501 HFGASASVGy QW\*

**FIG. 14C**

52 TDETGLINV ETEKLSFGAN GKKVNIISdT KGLNFAKETA GTNGDttVHL  
 101 NGIGSTLTDM LLNTGATTNV TNDNVTdDEK KRAASVKDVL NAGWNIKGVK  
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA  
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA  
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMDet VNINAGNNIE  
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP  
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA  
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR  
 501 GHFGASASVG YQW\*

**FIG. 14D**

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK  
 101 DGKLVGTGDK GENGSSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG  
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ  
 201 LQNSGWNLDK KAVAGSSGKV ISGNVSPSKG KMDET VNINA GNNIEITRNG  
 251 KNIDIATSM T PQFSSVSLGA GADAP T LSVD GDALNVGSKK DNKPVRITNV  
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY  
 351 LPGKSMMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS  
 401 ASVG YQW\*

### FIG. 14E

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT  
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGLK VTGKDKGENG SSTDEGEGLV  
 151 TAKEVIDAVN KAGWRMKT TTT ANGQTGQADK FETVTSGTNV TFASGKGTTA  
 201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDKAVA GSSGKVISGN  
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA  
 301 PTLSDVDGAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN  
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMAIGGGTY RGEAGYAIGY  
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW\*

### FIG. 14F

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKNITS DTK  
 101 GLNFAKETAG TNGD TTVHLN GIGSTLT DRA ASVKDVLNAG WNIKGVKNVD  
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEKDGLV  
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT TTA NGQTGQADKF  
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG  
 301 WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE ITRNGKNIDI  
 351 ATSMTPQFSS VSLGAGADAP T LSV DGDALN VGSKKDNKPV RITNVAPGVK  
 401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS  
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVG Y  
 501 QW\*

### FIG. 14G